

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 10, 2004, 11:42:46 ; Search time 25.814 Seconds
(without alignments)
38.536 Million cell updates/sec

Title: US-10-036-418-2

Sequence: 1 IGLHDPHSHGTLPNGS 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
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3: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
4: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/BACKFILE1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	174	2	US-08-401-530A-2
2	85	100.0	174	2	US-08-709-662-6
3	85	100.0	175	1	US-08-909-725-6
4	63	74.1	174	1	US-07-778-156-7
5	63	74.1	174	2	US-08-822-261-4
6	63	74.1	174	2	US-08-422-166-7
7	63	74.1	174	4	US-09-226-852-4
8	63	74.1	175	2	US-08-464-537-2
9	63	74.1	175	2	US-08-401-530A-4
10	63	74.1	175	2	US-08-709-662-4
11	63	74.1	175	2	US-08-822-261-3
12	63	74.1	175	2	US-09-226-852-3
13	54	63.5	175	2	US-08-822-261-1
14	54	63.5	175	4	US-09-226-852-1
15	53	62.4	158	1	US-07-778-156-3
16	53	62.4	158	2	US-08-422-166-3
17	53	62.4	175	2	US-08-401-530A-3
18	53	62.4	175	2	US-08-709-662-3
19	53	62.4	184	1	US-07-778-156-2
20	53	62.4	184	2	US-08-422-166-2
21	49	57.6	208	3	US-09-103-478-2
22	49	57.6	208	3	US-09-193-931C-2
23	49	57.6	208	4	US-09-026-221-2
24	49	57.6	208	4	US-09-533-029-70
25	48	56.5	208	4	US-09-516-052-2
26	48	56.5	174	2	US-08-401-530A-5
27	48	56.5	174	2	US-08-401-530A-6

28	48	56.5	174	2	US-08-709-662-5	Sequence 5, Appl1
29	48	56.5	174	2	US-08-709-662-6	Sequence 6, Appl1
30	48	56.5	251	4	US-09-602-787A-480	Sequence 480, App
31	48	56.5	595	4	US-09-489-039A-13433	Sequence 13433, A
32	47	55.3	359	4	US-09-540-236-2472	Sequence 2472, Ap
33	45	52.9	100	3	US-09-177-249-246	Sequence 246, App
34	43	50.6	216	4	US-09-270-767-44019	Sequence 44019, A
35	43	50.6	221	4	US-09-270-767-44019	Sequence 44019, A
36	42	49.4	372	3	US-08-998-416-4	Sequence 4, Appl1
37	42	49.4	379	4	US-09-248-796A-18277	Sequence 18277, A
38	42	49.4	447	1	US-08-365-689-1	Sequence 1, Appl1
39	42	49.4	447	1	US-07-747-781-1	Sequence 1, Appl1
40	42	49.4	447	1	US-08-145-138A-1	Sequence 1, Appl1
41	42	49.4	447	5	PCT-US92-06888-1	Sequence 1, Appl1
42	42	49.4	447	5	PCT-US93-03027-5	Sequence 5, Appl1
43	42	49.4	774	3	US-09-346-237-8	Sequence 8, Appl1
44	42	49.4	899	1	US-08-365-689-2	Sequence 2, Appl1
45	42	49.4	899	1	US-08-145-138A-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-401-530A-2
Sequence 2, Application US/08401530A
Patent No. 5834590
GENERAL INFORMATION:
APPLICANT: Vink, Aaron I.
APPLICANT: Pittenger, Gary L.
APPLICANT: Rataeioff, Ronit
APPLICANT: Rosenbery, Lawrence
APPLICANT: Duguid, William P.
TITLE OF INVENTION: INGP PROTEIN INVOLVED IN PANCREATIC
TITLE OF INVENTION: ISLET NEOGENESIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: US
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,530A
FILING DATE: 22-FEB-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 00570,48743
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9108
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-401-530A-2

Query Match 100.0%; Score 85; DB 2; Length 174;
Best local similarity 100.0%; Pred. No. 3.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 IGLHDPHSHGTLPNGS 15
|||||

Db 103 IGLHDPHSHGLTPNGS 117

RESULT 2

US-08-709-662-2
Sequence 2, Application US/08709662
Patent No. 5840531

GENERAL INFORMATION:

APPLICANT: Vink, Aaron I.
APPLICANT: Pitterenger, Gary L.
APPLICANT: Rafalooff, Ronit
APPLICANT: Rosenbergs, Lawrence
APPLICANT: Duguid, William P.
TITLE OF INVENTION: INAP PROTEIN INVOLVED IN PANCREATIC
TITLE OF INVENTION: IL2R NEOGENESIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: US
ZIP: 20001-4597

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,662
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 00570.59178
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-709-662-2

Query Match 100.0%; Score 85; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IGLHDPHSHGLTPNGS 15
Db 103 IGLHDPHSHGLTPNGS 117

RESULT 3

US-08-909-725-6
Sequence 6, Application US/08909725
Patent No. 5804421

GENERAL INFORMATION:

APPLICANT: Vink, Aaron
APPLICANT: Pitterenger, Gary
APPLICANT: Rafalooff-phail, Ronit
APPLICANT: Barlow, Scott
TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF
TITLE OF INVENTION: INAP IN BACTERIAL AND EUKARYOTIC CELLS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: DC

COUNTRY: USA

ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/909,725

FILING DATE: 12-03-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/741,096

FILING DATE: 30-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Kagan, Sarah A

REGISTRATION NUMBER: 32,145

REFERENCE/DOCKET NUMBER: 0570.05173

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9100

TELEFAX: 202-508-9299

TELEX: 97430 BMB UT

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 175 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-909-725-6

Query Match 100.0%; Score 85; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IGLHDPHSHGLTPNGS 15
Db 104 IGLHDPHSHGLTPNGS 118

RESULT 4

US-07-778-156-7
Sequence 7, Application US/07778156
Patent No. 5436169

GENERAL INFORMATION:

APPLICANT: IOVANNA, JUAN-LUCIO
APPLICANT: KEIM, VOLKER
APPLICANT: DAGORN, JEAN-CHARLES
TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
TITLE OF INVENTION: PANCREATITIS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBION, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/778,156

FILING DATE: 19911219

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Obion, No. 5436169man F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 354-012-0 PCT

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OM protein - protein search, using sw model

Run on: December 10, 2004, 11:47:11 ; Search time 278.698 Seconds
(without alignments)
55.659 Million cell updates/sec

Title: US-10-036-418-4

Sequence: 1 OKSGFQMRDENCE 14

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 6730630 seqs, 1107998698 residues

Total number of hits satisfying chosen parameters: 6730630

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Pending Patents AA Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	84	100.0	14	26 US-10-036-418-4	Sequence 4, Appl
3	84	100.0	14	29 US-10-376-046-3	Sequence 3, Appl
4	84	100.0	145	1 PCT-US02-27637-23	Sequence 23, Appl
5	84	100.0	145	1 PCT-US03-26779-23	Sequence 23, Appl
6	84	100.0	145	28 US-10-231-494-23	Sequence 23, Appl
7	84	100.0	145	36 US-60-485-404-23	Sequence 23, Appl
8	84	100.0	148	1 PCT-US02-27637-21	Sequence 21, Appl
9	84	100.0	148	1 PCT-US03-26779-21	Sequence 21, Appl
10	84	100.0	148	28 US-10-231-494-21	Sequence 21, Appl
11	84	100.0	148	36 US-60-485-404-21	Sequence 21, Appl
12	84	100.0	171	1 PCT-US02-40892-840	Sequence 840, App
13	84	100.0	171	1 PCT-US02-40892A-840	Sequence 13606, A
14	84	100.0	171	22 US-09-791-537-13606	Sequence 840, App
15	84	100.0	171	33 US-10-775-180-840	Sequence 840, App
16	84	100.0	174	1 PCT-US02-27637-17	Sequence 17, Appl
17	84	100.0	174	1 PCT-US03-26779-17	Sequence 17, Appl
18	84	100.0	174	1 PCT-US96-01528-2	Sequence 2, Appl
19	84	100.0	174	8 US-08-401-530-2	Sequence 2, Appl
20	84	100.0	174	11 US-08-741-096A-6	Sequence 6, Appl
21	84	100.0	174	21 US-09-717-095-2	Sequence 2, Appl
22	84	100.0	174	28 US-10-231-494-17	Sequence 17, Appl
23	84	100.0	174	30 US-10-421-363-3	Sequence 3, Appl
24	84	100.0	174	30 US-10-421-363-3	Sequence 3, Appl
25	84	100.0	174	36 US-60-485-404-17	Sequence 17, Appl
26	84	100.0	175	1 PCT-US02-27637-19	Sequence 2, Appl
27	84	100.0	175	1 PCT-US03-06221-2	Sequence 2, Appl
28	84	100.0	175	1 PCT-US03-26779-19	Sequence 19, Appl
29	84	100.0	175	11 US-08-741-096B-6	Sequence 6, Appl
30	84	100.0	175	22 US-09-659-379-6	Sequence 6, Appl
31	84	100.0	175	22 US-09-791-537-62734	Sequence 62734, A
32	84	100.0	175	28 US-10-231-494-19	Sequence 19, Appl
33	84	100.0	175	28 US-10-253-733-1	Sequence 2, Appl
34	84	100.0	175	29 US-10-376-046-2	Sequence 2, Appl
35	84	100.0	175	36 US-60-485-404-19	Sequence 19, Appl
36	84	100.0	175	32 US-09-791-537-62734	Sequence 62734, A
37	61	72.6	175	22 US-09-791-537-114187	Sequence 114187, A
38	56	66.7	121	1 PCT-US01-08631-49046	Sequence 49046, A
39	56	66.7	129	1 PCT-US02-27143-29	Sequence 29, Appl
40	56	66.7	129	27 PCT-US02-27143-45	Sequence 45, Appl
41	56	66.7	129	27 US-10-170-205E-8573	Sequence 8573, Ap
42	56	66.7	129	30 US-10-487-078-29	Sequence 29, Appl
43	56	66.7	129	30 US-10-487-078-45	Sequence 45, Appl
44	56	66.7	147	1 PCT-US03-28227-3101	Sequence 3101, Ap
45	56	66.7	169	36 US-60-242-679-1089	Sequence 1089, Ap

Although 100%
All are lengths 174-
175

Where no applicant
see spec 12-204-2

RESULT 1
PCT-US03-06221-3
Sequence 3, Application PC/TUS0306221
GENERAL INFORMATION:
APPLICANT: GMP Endotherapeutics, Inc.
APPLICANT: Vinik, Aaron I.
TITLE OF INVENTION: Assay for Anti-INGAP Antibodies
FILE REFERENCE: 9057HLS/VB
CURRENT APPLICATION NUMBER: PCT/US03/06221
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: U.S. 60/361,040
PRIOR FILING DATE: 2003-03-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 14
TYPE: PRT
ORGANISM: hamster sp.
PCT-US03-06221-3

Query Match 100.0%; Score 84; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKSGFQKWRDPNCE 14
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DB 1 QKSGFQKWRDPNCE 14

RESULT 2
US-10-036-418-4
; Sequence 4, Application US/10036418
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron

; APPLICANT: Taylor-Fishwick, David
; TITLE OF INVENTION: INGA Displacement Assay
; FILE REFERENCE: 005126.00009
; CURRENT APPLICATION NUMBER: US/10/036,418
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,210
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Cricetus
US-10-036-418-4

Query Match 100.0%; Score 84; DB 26; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKSGFQKWRDPNCE 14
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DB 1 QKSGFQKWRDPNCE 14

2003016631

RESULT 3
US-10-376-046-3
; Sequence 3, Application US/10376046
; GENERAL INFORMATION:
; APPLICANT: GMP Endotherapeutics, Inc.
; APPLICANT: Vinik, Aaron I.
; APPLICANT: Taylor-Fishwick, David A.
; TITLE OF INVENTION: Assay for Anti-INGAP Antibodies
; FILE REFERENCE: 9057#L5
; CURRENT APPLICATION NUMBER: US/10/376,046
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: U.S. 60/361,040
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 14
; TYPE: PRT
; ORGANISM: hamster sp.
US-10-376-046-3

Query Match 100.0%; Score 84; DB 29; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKSGFQKWRDPNCE 14
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DB 1 QKSGFQKWRDPNCE 14

RESULT 4
PCT-US02-27637-23
; Sequence 23, Application PC/TUS0227637
; GENERAL INFORMATION:

; APPLICANT: Prior, Christopher P.
; TITLE OF INVENTION: Modified Transferrin Fusion Proteins
; FILE REFERENCE: 54710-5001-WO
; CURRENT APPLICATION NUMBER: PCT/US02/27637
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: INGA
PCT-US02-27637-23

Query Match 100.0%; Score 84; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKSGFQKWRDPNCE 14
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DB 121 QKSGFQKWRDPNCE 134

RESULT 5
PCT-US03-26779-23
; Sequence 23, Application PC/TUS0326779
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; APPLICANT: Turner, Andrew J.
; APPLICANT: Sadeghi, Homayoun
; TITLE OF INVENTION: Transferrin Fusion Protein Libraries
; FILE REFERENCE: 054710-5007-WO
; CURRENT APPLICATION NUMBER: PCT/US03/26779
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 10/384,060
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 60/485,404
; PRIOR FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: INGA
PCT-US03-26779-23

Query Match 100.0%; Score 84; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKSGFQKWRDPNCE 14
|||||
DB 121 QKSGFQKWRDPNCE 134

RESULT 6
US-10-231-494-23
; Sequence 23, Application US/10231494
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; TITLE OF INVENTION: Modified Transferrin Fusion Proteins
; FILE REFERENCE: 54710-5001-US

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 10, 2004, 11:57:22 ; Search time 81.7209 Seconds
(without alignments)
61.190 Million cell updates/sec

Title: US-10-036-418-3

Perfect score: 71

Sequence: 1 IADRGYCAVLSQK 14

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA*
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3: /cgn2_6/ptodata/1/pubpaa/US05_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US04_PUBCOMB.pep:*
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10: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/1/pubpaa/US05_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US04_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US03_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US00_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	100.0	14	US-10-036-418-3	Sequence 3, Appli
2	71	14	US-10-376-046-4	Sequence 2, Appli
3	71	14	US-10-231-494-23	Sequence 23, Appli
4	71	14	US-10-231-494-21	Sequence 21, Appli
5	71	14	US-10-421-363-3	Sequence 3, Appli
6	71	14	US-10-231-494-17	Sequence 17, Appli
7	71	14	US-10-469-314-2	Sequence 2, Appli
8	71	14	US-10-376-046-2	Sequence 2, Appli
9	71	14	US-10-231-494-19	Sequence 19, Appli
10	71	14	US-10-253-733-1	Sequence 201225
11	63.4	78	US-10-425-115-201225	Sequence 25, Appli
12	60.6	70	US-10-264-480-25	Sequence 26, Appli
13	60.6	70	US-10-264-480-26	Sequence 26, Appli

14	43	60.6	382	14	US-10-346-144-7	Sequence 7, Appli
15	43	60.6	724	14	US-10-346-144-5	Sequence 5, Appli
16	42	59.2	366	14	US-10-437-963-106270	Sequence 106270
17	41	57.7	163	15	US-10-424-599-217941	Sequence 217941
18	40	56.3	71	9	US-09-894-882-119	Sequence 119, Appli
19	40	56.3	260	15	US-10-240-363A-5	Sequence 5, Appli
20	40	56.3	325	9	US-09-738-625-4643	Sequence 4643, Ap
21	40	56.3	338	14	US-10-156-761-10747	Sequence 10747, A
22	40	56.3	370	15	US-10-424-599-208486	Sequence 208486
23	40	56.3	1626	17	US-10-425-115-276948	Sequence 276948
24	39	54.9	175	14	US-10-028-248A-111	Sequence 111, App
25	39	54.9	175	15	US-10-107-782-111	Sequence 111, App
26	39	54.9	192	16	US-10-767-701-56127	Sequence 56127, A
27	39	54.9	204	15	US-10-424-599-211047	Sequence 211044, A
28	39	54.9	335	15	US-10-282-122A-51097	Sequence 51097, A
29	39	54.9	1292	16	US-10-437-963-198709	Sequence 198709
30	38	53.5	56	17	US-10-425-115-284026	Sequence 284026
31	38	53.5	94	17	US-10-425-115-308046	Sequence 308046
32	38	53.5	328	16	US-10-437-963-175648	Sequence 175648
33	38	53.5	446	17	US-10-739-930-9850	Sequence 9850, Ap
34	38	53.5	447	14	US-10-314-657-33	Sequence 33, Appli
35	38	53.5	454	14	US-10-369-493-23078	Sequence 23078, A
36	38	53.5	950	16	US-10-437-963-175646	Sequence 175646
37	38	53.5	1222	15	US-10-282-122A-69799	Sequence 69799, A
38	37	52.1	52	15	US-10-424-599-258805	Sequence 258805
39	37	52.1	73	9	US-09-864-761-37918	Sequence 37918, A
40	37	52.1	158	17	US-10-425-115-283615	Sequence 283615
41	37	52.1	169	14	US-10-238-075-967	Sequence 967, App
42	37	52.1	191	15	US-10-425-114-48236	Sequence 48236, A
43	37	52.1	199	15	US-10-425-114-53496	Sequence 53496, A
44	37	52.1	201	17	US-10-425-115-254956	Sequence 254956
45	37	52.1	202	15	US-10-282-122A-54259	Sequence 54259, A

ALIGNMENTS

RESULT 1
US-10-036-418-3
Sequence 3, Application US/10036418
Publication No. US20020127624A1
GENERAL INFORMATION:
APPLICANT: Vianik, Aaron
TITLE OF INVENTION: INGAP Displacement Assay
FILE REFERENCE: 005126 00009
CURRENT APPLICATION NUMBER: US/10/036,418
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: 60/260,210
PRIOR FILING DATE: 2000-01-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 14
TYPE: PRT
ORGANISM: Cricetus
US-10-036-418-3

Query Match 100.0%; Score 71; DB 13; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IADRGYCAVLSQK 14

Db 1 IADRGYCAVLSQK 14

US-10-376-046-4

US-10-376-046-4

US-10-376-046-4
Sequence 2, Appli
Publication No. US20030166031A1
GENERAL INFORMATION:
APPLICANT: GMP Endotherapeutics, Inc.

APPLICANT: Vinik, Aaron I.
APPLICANT: Taylor-Fishwick, David A.
TITLE OF INVENTION: Assay for Anti-INGAP Antibodies
FILE REFERENCE: 9057#L5
CURRENT APPLICATION NUMBER: US/10/376,046
CURRENT FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: U.S. 60/361,040
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 14
TYPE: PRT
ORGANISM: hamster sp.
US-10-376-046-4

Query Match 100.0%; Score 71; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IAADRGCAVL50K 14
Db 1 IAADRGCAVL50K 14

RESULT 3
US-10-231-494-23
Sequence 23, Application US/10231494
Publication No. US20040023334A1
GENERAL INFORMATION:
APPLICANT: Prior, Christopher P.
TITLE OF INVENTION: Modified Transferrin Fusion Proteins
FILE REFERENCE: 54710-5001-US
CURRENT APPLICATION NUMBER: US/10/231,494
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 60/315,745
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: US 60/334,059
PRIOR FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 23
LENGTH: 145
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: INGAP
US-10-231-494-23

Query Match 100.0%; Score 71; DB 15; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IAADRGCAVL50K 14
Db 109 IAADRGCAVL50K 122

RESULT 4
US-10-231-494-21
Sequence 21, Application US/10231494
Publication No. US20040023334A1
GENERAL INFORMATION:
APPLICANT: Prior, Christopher P.
TITLE OF INVENTION: Modified Transferrin Fusion Proteins
FILE REFERENCE: 54710-5001-US
CURRENT APPLICATION NUMBER: US/10/231,494
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 60/315,745
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: US 60/334,059
PRIOR FILING DATE: 2001-11-30

NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGTH: 148
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: INGAP
US-10-231-494-21

Query Match 100.0%; Score 71; DB 15; Length 148;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IAADRGCAVL50K 14
Db 111 IAADRGCAVL50K 124

RESULT 5
US-10-421-363-3
Sequence 3, Application US/10421363
Publication No. US20040018623A1
GENERAL INFORMATION:
APPLICANT: Rosenberg, Lawrence
TITLE OF INVENTION: MEDIUM FOR PREPARING DIFFERENTIATED
CELLS
FILE REFERENCE: 701826-05621-CIP
CURRENT APPLICATION NUMBER: US/10/421,363
CURRENT FILING DATE: 2003-04-23
PRIOR APPLICATION NUMBER: US 10/111,485
PRIOR FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: PCT/CA00/01284
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/162,137
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 174
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: INGAP translated Protein
US-10-421-363-3

Query Match 100.0%; Score 71; DB 15; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IAADRGCAVL50K 14
Db 138 IAADRGCAVL50K 151

RESULT 6
US-10-231-494-17
Sequence 17, Application US/10231494
Publication No. US20040023334A1
GENERAL INFORMATION:
APPLICANT: Prior, Christopher P.
TITLE OF INVENTION: Modified Transferrin Fusion Proteins
FILE REFERENCE: 54710-5001-US
CURRENT APPLICATION NUMBER: US/10/231,494
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 60/315,745
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: US 60/334,059
PRIOR FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 15, 2004, 14:37:36 ; Search time 154 Seconds
(without alignments)
48.918 Million cell updates/sec

Title: US-10-036-418-1

Perfect score: 111
Sequence: 1 FLSWVEGSESKKLPSSRITC 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 3: geneseqp20008:*
- 4: geneseqp20018:*
- 5: geneseqp20028:*
- 6: geneseqp20038:*
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- 8: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	111	100.0	21	ABD79542 Hamster I
2	111	100.0	171	ADH22043 Golden ha
3	111	100.0	174	AAR98525 Hamster i
4	111	100.0	174	ABE79915 Hamster i
5	111	100.0	174	ABE72830 Human ING
6	111	100.0	174	ADL70746 Human ING
7	111	100.0	175	AAM64790 Human ING
8	111	100.0	175	ABP72831 Human ING
9	111	100.0	175	ADCL3872 Hamster i
10	111	100.0	175	ADL70748 Human ING
11	71	64.0	175	AAR95089 Reg-2 pro
12	71	64.0	175	AAI18614 Amino aci
13	71	64.0	175	ADB83454 Rat Prote
14	71	64.0	184	AAI14797 Rat pancer
15	68	61.3	129	ABG18687 Novel hum
16	68	61.3	129	ABR56770 Human sec
17	68	61.3	129	ABR56754 Human sec
18	68	61.3	174	AAI14795 Fragment
19	68	61.3	175	AAI57117 Human Pan
20	68	61.3	175	AAI54098 Mouse PAP
21	68	61.3	175	AAW71682 Human pan
22	68	61.3	175	AAW41755 Human PRO
23	68	61.3	175	AAI44311 Human PRO
24	68	61.3	175	AAI29235 Human PRO
25	68	61.3	175	ABD84876 Human PRO

26	68	61.3	175	5	ABU10605	AbJ10605 Human nov
27	68	61.3	175	5	ABE95482	ABE95482 Human ang
28	68	61.3	175	6	ABU58611	ABU58611 Human PRO
29	68	61.3	175	6	ABU88159	ABU88159 Novel hum
30	68	61.3	175	6	ABU84474	ABU84474 Human sec
31	68	61.3	175	6	ABR66348	ABR66348 Human sec
32	68	61.3	175	6	ABR65738	ABR65738 Human sec
33	68	61.3	175	6	ABU99678	ABU99678 Human sec
34	68	61.3	175	6	ABU82917	ABU82917 Human PRO
35	68	61.3	175	6	ABU90038	ABU90038 Novel hum
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38	68	61.3	175	6	ABU92771	ABU92771 Human sec
39	68	61.3	175	6	ABO08848	ABO08848 Human sec
40	68	61.3	175	6	ABO02900	ABO02900 Human sec
41	68	61.3	175	6	ABR75054	ABR75054 Human sec
42	68	61.3	175	6	ABR94816	ABR94816 Human sec
43	68	61.3	175	6	ABO25257	ABO25257 Novel hum
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ALIGNMENTS

RESULT 1
ABD79542
ID ABD79542 standard; peptide; 21 AA.

XX ABD79542;
01-OCT-2002 (first entry)

XX Hamster islet neogenesis associated protein (INGAP) immunogen.

XX Islet neogenesis associated protein; INGAP; immunogen; hamster; pancreas;
diabetes; immunoassay.

XX Cricetulus sp.
WO200256028-A2.

XX 18-JUL-2002.

XX 08-JAN-2002; 2002WO-US000071.

XX 09-JAN-2001; 2001US-0260210P.
XX 07-JAN-2002; 2002US-00036418.

XX (GMPF-) GMP ENDOTHERAPUTICS INC.

XX Vink AI, Taylor-Fishwick D;
WPI; 2002-557841/59.

XX Assaying islet neogenesis associated protein (INGAP) for treating
diabetes types I and II, comprises determining the amount of labeled
INGAP molecule bound to antibodies or to a solid support comprising the
bound antibodies.

XX Claim 1; Page 12; 29pp; English.

XX The present sequence is a peptide immunogen corresponding to amino acid
residues 20-40 of full-length hamster islet neogenesis associated protein
(INGAP). The invention provides methods for assaying INGAP in a test
sample, in a competitive binding assay, antibodies which specifically
bind to the INGAP immunogen are contacted with a test sample which may
contain INGAP protein, and a labeled INGAP molecule, e.g. a fusion
protein comprising INGAP protein and a marker protein. The amount of
labeled INGAP molecule bound to the antibodies is determined. This
amount is inversely related to INGAP protein in the test sample.
XX Antibodies raised against different INGAP immunogens (see ABD79543-45)
and their subfragments may also be used. They may be monoclonal or

polyclonal, may be bound to a solid support, and do not specifically bind to other portions of the INAP protein or to other human proteins. The method can be used to determine the amount of INAP e.g. in culture media or biological tissues and fluids. The ability to assay INAP will facilitate the full exploitation of this protein for fighting human disease, such as diabetes types I and II

SO Sequence 21 AA;

Query Match 100.0%; Score 111; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSWVEGESOKKLPSSRLTC 21
1 FLSWVEGESOKKLPSSRLTC 21

ADH22043

ID ADH22043 standard; peptide; 171 AA.

AC ADH22043;

DT 11-MAR-2004 (first entry)

XX Golden hamster INAP peptide, SEQ ID NO:840.

XX Fusion protein; human serum albumin; HSA; therapeutic protein;
XX shelf-life; in vitro biological activity; in vivo biological activity;
XX metabolic disorder; endocrine disorder; diabetes; type 1; type 2;
XX diabetes-related condition; hyperglycaemia; neural disorder; neuropathy;
XX retinopathy; cardiovascular disorder; heart disease; renal disorder;
XX obesity; glucose level maintenance; weight loss; antidiabetic; cardiant;
XX anorectic; ophthalmological; gene therapy; INAP; golden hamster.

OS Mesocricetus auratus.

XX WO2003059934-A2.

PD 24-JUL-2003.

23-DEC-2002; 2002WO-US040892.

PR 21-DEC-2001; 2001US-0341811P.

PR 24-JAN-2002; 2002US-0350358P.

PR 26-FEB-2002; 2002US-0359370P.

PR 28-FEB-2002; 2002US-0360000P.

PR 27-MAR-2002; 2002US-0367500P.

PR 08-APR-2002; 2002US-0370227P.

PR 10-MAY-2002; 2002US-0378850P.

PR 24-JUL-2002; 2002US-0398008P.

PR 09-AUG-2002; 2002US-0402131P.

PR 13-AUG-2002; 2002US-0402708P.

PR 18-SEP-2002; 2002US-0411355P.

PR 02-OCT-2002; 2002US-0414984P.

PR 11-OCT-2002; 2002US-0417611P.

PR 23-OCT-2002; 2002US-0420246P.

PR 05-NOV-2002; 2002US-0423623P.

PA (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA Haseltine WA;

XX WPI; 2003-598501/56.

XX New albumin fusion protein, useful for preparing a composition for
PT treating diabetes mellitus.

XX Disclosure; SEQ ID NO 840; 1086pp; English.

XX The invention relates to fusion proteins comprising human serum albumin
CC (ADH21530) and a therapeutic polypeptide such as a therapeutic protein,

CC antibody or peptide or their variants or fragments. The therapeutic
CC protein may be fused to the N-terminus, the C-terminus or both termini of
CC albumin via a linker. The albumin component of the fusion proteins
CC prolongs the shelf-life and the in vitro and vivo biological activity of
CC the proteins compared with those of the corresponding therapeutic
CC proteins on their own. The invention also relates to nucleic acids
CC encoding albumin fusion proteins, vectors and host cells comprising an
CC albumin fusion protein nucleic acid, compositions and kits comprising an
CC albumin fusion protein, the method of extending the shelf-life of a
CC therapeutic protein by fusion with albumin, and the treatment of disease
CC using an albumin fusion protein. The albumin fusion proteins may be used
CC in the treatment of metabolic/endocrine disorders, diabetes and diabetes-
CC related conditions. Specifically the albumin fusion proteins may be used
CC to treat type 1 and type 2 diabetes, hyperglycaemia, neural disorders
CC (especially neuropathy), retinopathy, cardiovascular disorders
CC (especially heart disease, renal disorders and obesity. The proteins may
CC also be used in a method of maintaining a basal glucose level in a
CC patient and in a method for losing weight. The present sequence is
CC related to the invention.

SO Sequence 171 AA;

Query Match 100.0%; Score 111; DB 7; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLSWVEGESOKKLPSSRLTC 21
16 FLSWVEGESOKKLPSSRLTC 36

DB 16 FLSWVEGESOKKLPSSRLTC 36

RESULT 3
AAR98525

ID AAR98525 standard; protein; 174 AA.

AC AAR98525;

DT 18-APR-1997 (first entry)

XX Hamster islet neogenesis associated protein.

XX Hamster; islet neogenesis associated protein; INAP; pancreas; endocrine;
XX proliferation; pancreatic tissue; cellophane; duct epithelium; homology;
XX differential display method; open reading frame; liver; adenocarcinoma;
XX pancreatitis associated protein; lithostathine; pancreatic stone protein;
XX beta-cell; regeneration; insulin; diabetes; mammal.

OS Cricetus sp.

XX WO9626215-A1.

PD 29-AUG-1996.

PR 12-FEB-1996; 96WO-US001528.

PR 22-FEB-1995; 95US-00401530.

PR 07-NOV-1995; 95US-0006271P.

PA (EVIR-) EASTERN VIRGINIA MEDICAL SCHOOL.

XX Vinik AL, Pittenger GL, Rafaeloff R, Rosenberg L, Duguid WP;

XX WPI; 1996-402318/40.

XX N-PSDB; AAT36612.

XX Mammalian islet neo:genesis associated protein - isolated by stimulating
PT mammalian pancreas by wrapping in cellophane, for treatment of diabetes,
PT etc.

XX Claim 2; Page 26; 50pp; English.

XX This is the amino acid sequence of the hamster islet neogenesis
CC associated protein (INAP). The gene is isolated from pancreatic cells